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PATENT

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AMENDMENTS TO THE CLAIMS

Please cancel claims 5-14 and 34-48, amend claims 21, 24 and 33, and add new claims 49-60 as follows.

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1 (Original). A method for identifying a modulator of binding and/or function between a DmGPCR1 and a DmGPCR1 binding partner, comprising the steps of : (a) contacting a DmGPCR1 binding partner and a composition comprising a DmGPCR1 in the presence or in the absence of a putative modulator compound; (b) detecting binding between the DmGPCR1 binding partner and the DmGPCR1 ; and (c) determining whether binding or function in the presence of said putative modulator compound is increased or decreased compared to binding or function in the absence of said putative modulator compound, wherein said DmGPCR1 binding partner has a sequence with at least 70% sequence identity to a sequence selected from the group consisting of SEQ ID NO: 186 and SEQ ID NO: 187.

2 (Original). The method according to claim 1, wherein said DmGPCR1 binding partner has a sequence with at least 80% sequence identity to a sequence selected from the group consisting of SEQ ID NO: 186 and SEQ ID NO: 187.

3 (Original). The method according to claim 1, wherein said DmGPCR1 binding partner has a sequence with at least 95% sequence identity to a sequence selected from the group consisting of SEQ ID NO: 186 and SEQ ID NO: 187.

4 (Original). The method according to claim 1, wherein said DmGPCR1 binding partner has a sequence selected from the group consisting of SEQ ID NO: 186 and SEQ ID NO: 187.

5-14. (Canceled)

15 (Original). A method of binding a DmGPCR with a DmGPCR binding partner comprising the steps of : contacting a composition comprising a DmGPCR with a DmGPCR binding partner; and allowing said DmGPCR binding partner to bind said DmGPCR.

16 (Original). A method according to claim 15, wherein said DmGPCR is DmGPCR5 (SEQ ID NO: 9).

17 (Original). A method according to claim 16, wherein said DmGPCR binding partner is a drotachykinin (DTK).

18 (Original). The method according to claim 17, wherein said drotachykinin has a sequence with at least 80% sequence identity to a sequence selected from the group consisting of DTK-1 (SEQ ID NO: 169), Met8-DTK-2 (SEQ ID NO: 170), DTK-2 (SEQ ID NO: 171), DTK-3 (SEQ ID NO: 172), DTK-4 (SEQ ID NO: 173), and DTK-5 (SEQ ID NO: 174).

19 (Original). The method according to claim 15, wherein said DmGPCR is DmGPCR7 (SEQ ID NO: 17).

20 (Original). The method according to claim 19, wherein said DmGPCR binding partner is a leucokinin (LK).

21 (Currently Amended). The method according to claim 20, wherein said leucokinin has a sequence with at least 80% sequence identity to a sequence selected from the group consisting of LK-I (SEQ ID NO: 175), LK-V (SEQ ID NO: 176), LK-VI (SEQ ID NO: 177), and LK-VIII (SEQ ID NO: 178), Culekinin (SEQ ID NO: 179), LY7MMaea lymnolcinin (SEQ ID NO: 180), DLK-1 (SEQ ID NO : 181), DLK-2 (SEQ ID NO: 182), and DLK-2a (SEQ ID NO: 183).

22 (Original). The method according to claim 15, wherein said DmGPCR is DmGPCR8 (SEQ ID NO: 19).

23 (Original). The method according to claim 22, wherein said DmGPCR binding partner is an allatostatin.

24 (Currently Amended). The method according to claim 23, wherein said allatostatin has a sequence with at least 80% sequence identity to a sequence selected from the group consisting of AST-C (SEQ ID NO: 184), ~~or~~ and DST-C (SEQ ID NO: 185).

25 (Original). A method for identifying a modulator of binding and/or function between a DmGPCR and a DmGPCR binding partner, comprising the steps of : contacting a DmGPCR binding partner and a composition comprising a DmGPCR in the presence or in the absence of a putative modulator compound; detecting binding between the DmGPCR binding partner and the DmGPCR ; and determining whether binding in the presence of said putative modulator compound is increased or decreased compared to binding in the absence of said putative modulator compound, determining whether function in the presence of said putative modulator compound is increased or decreased compared to function in the absence of said putative modulator compound, wherein said DmGPCR is DmGPCR5 (SEQ ID NO: 9).

26 (Original). The method according to claim 25, wherein said DmGPCR binding partner is a drotachykinin.

27 (Original). The method according to claim 26, wherein said drotachykinin has a sequence with at least 80% sequence identity to a sequence selected from the group consisting of DTK-1 (SEQ ID NO: 169), Met8-DTK-2 (SEQ ID NO: 170), DTK-2 (SEQ ID NO: 171), DTK-3 (SEQ ID NO: 172), DTK-4 (SEQ ID NO: 173), and DTK-5 (SEQ ID NO: 174).

28 (Original). A method for identifying a modulator of binding and/or function between a DmGPCR and a DmGPCR binding partner, comprising the steps of : contacting a DmGPCR binding partner and a composition comprising a DmGPCR in the presence or in the absence of a putative modulator compound; detecting binding between the DmGPCR binding partner and the DmGPCR ; and determining whether binding in the presence of said putative

modulator compound is increased or decreased compared to binding in the absence of said putative modulator compound, determining whether function in the presence of said putative modulator compound is increased or decreased compared to function in the absence of said putative modulator compound, wherein said DmGPCR is DmGPCR7 (SEQ ID NO: 17).

29 (Original). The method according to claim 28, wherein said DmGPCR binding partner is a leucokinin.

30 (Original). The method according to claim 29, wherein said leucokinin has a sequence with at least 80% sequence identity to a sequence selected from the group consisting of LK-I (SEQ ID NO: 175), LK-V (SEQ ID NO: 176), LK-VI (SEQ ID NO: 177), LK-VIII (SEQ ID NO: 178), Culekinin (SEQ ID NO: 179), Ly7linaea lymnokinin (SEQ ID NO: 180), DLK-1 (SEQ ID NO: 181), DLK-2 (SEQ ID NO: 182), and DLK-2a (SEQ ID NO: 183).

31 (Original). A method for identifying a modulator of binding and/or function between a DmGPCR and a DmGPCR binding partner, comprising the steps of : contacting a DmGPCR binding partner and a composition comprising a DmGPCR, in the presence or in the absence of a putative modulator compound; detecting binding between the DmGPCR binding partner and the DmGPCR ; and determining whether binding in the presence of said putative modulator compound is increased or decreased compared to binding in the absence of said putative modulator compound, determining whether function in the presence of said putative modulator compound is increased or decreased compared to function in the absence of said putative modulator compound, wherein said DmGPCR is DmGPCR8 (SEQ ID NO: 19).

32 (Original). The method according to claim 31, wherein said DmGPCR binding partner is an allatostatin.

33 (Currently Amended). The method according to claim 32, wherein said allatostatin has a sequence with at least 80% sequence identity to a sequence selected from the group consisting of AST-C (SEQ ID NO: 184) ~~or~~ and DST-C (SEQ ID NO: 185).

34-48 (Canceled).

49 (New). A method for identifying a modulator of binding and/or function between a DmGPCR and a DmGPCR binding partner, comprising the steps of :

(a) contacting a DmGPCR1 binding partner and a composition comprising a DmGPCR in the presence or in the absence of a putative modulator compound;

(b) detecting binding between the DmGPCR binding partner and the DmGPCR; and

(c) determining whether binding or function in the presence of said putative modulator compound is increased or decreased compared to binding or function in the absence of said putative modulator compound,

wherein said DmGPCR and said DmGPCR binding partner are selected from the group consisting of:

DmGPCR1 and a DmGPCR1 binding partner has a sequence with at least 70% sequence identity to a sequence selected from the group consisting of SEQ ID NO:186 and SEQ ID NO:187;

DmGPCR5 and a drotachykinin;

DmGPCR7 and a leucokinin; and

DmGPCR8 and an allatostatin.

50 (New). The method of claim 49 wherein said DmGPCR and said DmGPCR binding partner are selected from the group consisting of:

DmGPCR1 and a DmGPCR1 binding partner has a sequence with at least 80% sequence identity to a sequence selected from the group consisting of SEQ ID NO:186 and SEQ ID NO:187;

DmGPCR5 and a drotachykinin that has a sequence with at least 80% sequence identity to a sequence selected from the group consisting of DTK-1 (SEQ ID NO:169), Met8-DTK-2 (SEQ ID NO:170), DTK-2 (SEQ ID NO:171), DTK-3 (SEQ ID NO:172), DTK-4 (SEQ ID NO:173), and DTK-5 (SEQ ID NO:174);

DmGPCR7 and a leucokinin that has a sequence with at least 80% sequence identity to a sequence selected from the group consisting of LK-I (SEQ ID NO:175), LK-V (SEQ ID NO:176), LK-VI (SEQ ID NO:177), LK-VIII (SEQ ID NO:178), Culekinin (SEQ ID NO: 179), Ly7linaea lymnokinin (SEQ ID NO:180), DLK-1 (SEQ ID NO:181), DLK-2 (SEQ ID NO:182), and DLK-2a (SEQ ID NO:183); and

DmGPCR8 and an allatostatin that has a sequence with at least 80% sequence identity to a sequence selected from the group consisting of AST-C (SEQ ID NO:184) and DST-C (SEQ ID NO:185).

51 (New). The method of claim 49 wherein said DmGPCR and said DmGPCR binding partner are selected from the group consisting of:

DmGPCR1 and a DmGPCR1 binding partner has a sequence with at least 90% sequence identity to a sequence selected from the group consisting of SEQ ID NO:186 and SEQ ID NO:187;

DmGPCR5 and a drotachykinin that has a sequence with at least 90% sequence identity to a sequence selected from the group consisting of DTK-1 (SEQ ID NO:169), Met8-DTK-2 (SEQ ID NO:170), DTK-2 (SEQ ID NO:171), DTK-3 (SEQ ID NO:172), DTK-4 (SEQ ID NO:173), and DTK-5 (SEQ ID NO:174);

DmGPCR7 and a leucokinin that has a sequence with at least 90% sequence identity to a sequence selected from the group consisting of LK-I (SEQ ID NO:175), LK-V (SEQ ID NO:176), LK-VI (SEQ ID NO:177), LK-VIII (SEQ ID NO:178), Culekinin (SEQ ID NO:179), Ly7linaea lymnokinin (SEQ ID NO:180), DLK-1 (SEQ ID NO:181), DLK-2 (SEQ ID NO:182), and DLK-2a (SEQ ID NO:183); and

DmGPCR8 and an allatostatin that has a sequence with at least 90% sequence identity to a sequence selected from the group consisting of AST-C (SEQ ID NO: 184) and DST-C (SEQ ID NO:185).

52 (New). The method of claim 49 wherein said DmGPCR and said DmGPCR binding partner are selected from the group consisting of:

DmGPCR1 and a DmGPCR1 binding partner has a sequence with at least 95% sequence identity to a sequence selected from the group consisting of SEQ ID NO: 186 and SEQ ID NO : 187;

DmGPCR5 and a drotachykinin that has a sequence with at least 95% sequence identity to a sequence selected from the group consisting of DTK-1 (SEQ ID NO:169), Met8-DTK-2 (SEQ ID NO:170), DTK-2 (SEQ ID NO:171), DTK-3 (SEQ ID NO:172), DTK-4 (SEQ ID NO:173), and DTK-5 (SEQ ID NO:174);

DmGPCR7 and a leucokinin that has a sequence with at least 95% sequence identity to a sequence selected from the group consisting of LK-I (SEQ ID NO:175), LK-V (SEQ ID NO:176), LK-VI (SEQ ID NO:177), LK-VIII (SEQ ID NO:178), Culekinin (SEQ ID NO:179), Ly7linaea lynmokinin (SEQ ID NO:180), DLK-1 (SEQ ID NO:181), DLK-2 (SEQ ID NO:182), and DLK-2a (SEQ ID NO:183); and

DmGPCR8 and an allatostatin that has a sequence with at least 95% sequence identity to a sequence selected from the group consisting of AST-C (SEQ ID NO:184) and DST-C (SEQ ID NO:185).

53 (New). The method of claim 49 wherein said DmGPCR and said DmGPCR binding partner are selected from the group consisting of:

DmGPCR1 and a DmGPCR1 binding partner has a sequence with at least 99% sequence identity to a sequence selected from the group consisting of SEQ ID NO: 186 and SEQ ID NO:187;

DmGPCR5 and a drotachykinin that has a sequence with at least 99% sequence identity to a sequence selected from the group consisting of DTK-1 (SEQ ID NO:169), Met8-DTK-2 (SEQ ID NO:170), DTK-2 (SEQ ID NO:171), DTK-3 (SEQ ID NO:172), DTK-4 (SEQ ID NO:173), and DTK-5 (SEQ ID NO:174);

DmGPCR7 and a leucokinin that has a sequence with at least 99% sequence identity to a sequence selected from the group consisting of LK-I (SEQ ID NO:175), LK-V (SEQ ID NO:176), LK-VI (SEQ ID NO:177), LK-VIII (SEQ ID NO: 178), Culekinin (SEQ ID NO:179), Ly7linaea lynmokinin (SEQ ID NO:180), DLK-1 (SEQ ID NO:181), DLK-2 (SEQ ID NO:182), and DLK-2a (SEQ ID NO:183); and

DmGPCR8 and an allatostatin that has a sequence with at least 99% sequence identity to a sequence selected from the group consisting of AST-C (SEQ ID NO:184) and DST-C (SEQ ID NO:185).

54 (New). The method of claim 49 wherein said DmGPCR and said DmGPCR binding partner are selected from the group consisting of:

DmGPCR1 and a DmGPCR1 binding partner has a sequence selected from the group consisting of SEQ ID NO:186 and SEQ ID NO:187;

DmGPCR5 and a drotachykinin that has a sequence selected from the group consisting of DTK-1 (SEQ ID NO:169), Met8-DTK-2 (SEQ ID NO:170), DTK-2 (SEQ ID NO:171), DTK-3 (SEQ ID NO:172), DTK-4 (SEQ ID NO:173), and DTK-5 (SEQ ID NO:174);

DmGPCR7 and a leucokinin that has a sequence selected from the group consisting of LK-I (SEQ ID NO:175), LK-V (SEQ ID NO:176), LK-VI (SEQ ID NO:177), LK-VIII (SEQ ID NO:178), Culekinin (SEQ ID NO:179), Ly7linaea lynmokinin (SEQ ID NO:180), DLK-1 (SEQ ID NO:181), DLK-2 (SEQ ID NO:182), and DLK-2a (SEQ ID NO:183); and

DmGPCR8 and an allatostatin that has a sequence selected from the group consisting of AST-C (SEQ ID NO:184) and DST-C (SEQ ID NO:185).

55 (New). The method according to claim 15, wherein said DmGPCR and said DmGPCR binding partner is selected from the group consisting of:

DmGPCR1 and a DmGPCR1 binding partner has a sequence with at least 70% sequence identity to a sequence selected from the group consisting of SEQ ID NO:186 and SEQ ID NO:187;

DmGPCR5 and a drotachykinin;

DmGPCR7 and a leucokinin; and

DmGPCR8 and an allatostatin.

56 (New). The method according to claim 15, wherein said DmGPCR and said DmGPCR binding partner is selected from the group consisting of:

DmGPCR1 and a DmGPCR1 binding partner has a sequence with at least 80% sequence identity to a sequence selected from the group consisting of SEQ ID NO:186 and SEQ ID NO:187;

DmGPCR5 and a drotachykinin that has a sequence with at least 80% sequence identity to a sequence selected from the group consisting of DTK-1 (SEQ ID NO:169), Met8-DTK-2 (SEQ ID NO:170), DTK-2 (SEQ ID NO:171), DTK-3 (SEQ ID NO:172), DTK-4 (SEQ ID NO:173), and DTK-5 (SEQ ID NO:174);

DmGPCR7 and a leucokinin that has a sequence with at least 80% sequence identity to a sequence selected from the group consisting of LK-I (SEQ ID NO:175), LK-V (SEQ ID NO:176), LK-VI (SEQ ID NO:177), LK-VIII (SEQ ID NO:178), Culekinin (SEQ ID NO:179), Ly7linaca lynmokinin (SEQ ID NO:180), DLK-1 (SEQ ID NO:181), DLK-2 (SEQ ID NO:182), and DLK-2a (SEQ ID NO:183); and

DmGPCR8 and an allatostatin that has a sequence with at least 80% sequence identity to a sequence selected from the group consisting of AST-C (SEQ ID NO:184) and DST-C (SEQ ID NO:185).

57 (New). The method according to claim 15, wherein said DmGPCR and said DmGPCR binding partner is selected from the group consisting of:

DmGPCR1 and a DmGPCR1 binding partner has a sequence with at least 90% sequence identity to a sequence selected from the group consisting of SEQ ID NO:186 and SEQ ID NO:187;

DmGPCR5 and a drotachykinin that has a sequence with at least 90% sequence identity to a sequence selected from the group consisting of DTK-1 (SEQ ID NO:169), Met8-DTK-2 (SEQ ID NO:170), DTK-2 (SEQ ID NO:171), DTK-3 (SEQ ID NO:172), DTK-4 (SEQ ID NO:173), and DTK-5 (SEQ ID NO:174);

DmGPCR7 and a leucokinin that has a sequence with at least 90% sequence identity to a sequence selected from the group consisting of LK-I (SEQ ID NO:175), LK-V (SEQ ID NO:176), LK-VI (SEQ ID NO:177), LK-VIII (SEQ ID NO:178), Culekinin (SEQ ID NO:179), Ly7linaea lynmokinin (SEQ ID NO:180), DLK-1 (SEQ ID NO:181), DLK-2 (SEQ ID NO:182), and DLK-2a (SEQ ID NO:183); and

DmGPCR8 and an allatostatin that has a sequence with at least 90% sequence identity to a sequence selected from the group consisting of AST-C (SEQ ID NO:184) and DST-C (SEQ ID NO:185).

58 (New). The method according to claim 15, wherein said DmGPCR and said DmGPCR binding partner is selected from the group consisting of:

DmGPCR1 and a DmGPCR1 binding partner has a sequence with at least 95% sequence identity to a sequence selected from the group consisting of SEQ ID NO:186 and SEQ ID NO:187;

DmGPCR5 and a drotachykinin that has a sequence with at least 95% sequence identity to a sequence selected from the group consisting of DTK-1 (SEQ ID NO:169), Met8-DTK-2 (SEQ ID NO:170), DTK-2 (SEQ ID NO:171), DTK-3 (SEQ ID NO:172), DTK-4 (SEQ ID NO:173), and DTK-5 (SEQ ID NO:174);

DmGPCR7 and a leucokinin that has a sequence with at least 95% sequence identity to a sequence selected from the group consisting of LK-I (SEQ ID NO:175), LK-V (SEQ ID NO:176), LK-VI (SEQ ID NO:177), LK-VIII (SEQ ID NO:178), Culekinin (SEQ

ID NO:179), Ly7linaea lymnokinin (SEQ ID NO:180), DLK-1 (SEQ ID NO:181), DLK-2 (SEQ ID NO:182), and DLK-2a (SEQ ID NO:183); and

DmGPCR8 and an allatostatin that has a sequence with at least 95% sequence identity to a sequence selected from the group consisting of AST-C (SEQ ID NO:184) and DST-C (SEQ ID NO:185).

59 (New). The method according to claim 15, wherein said DmGPCR and said DmGPCR binding partner is selected from the group consisting of:

DmGPCR1 and a DmGPCR1 binding partner has a sequence with at least 99% sequence identity to a sequence selected from the group consisting of SEQ ID NO:186 and SEQ ID NO:187;

DmGPCR5 and a drotachykinin that has a sequence with at least 99% sequence identity to a sequence selected from the group consisting of DTK-1 (SEQ ID NO:169), Met8-DTK-2 (SEQ ID NO:170), DTK-2 (SEQ ID NO:171), DTK-3 (SEQ ID NO:172), DTK-4 (SEQ ID NO:173), and DTK-5 (SEQ ID NO:174);

DmGPCR7 and a leucokinin that has a sequence with at least 99% sequence identity to a sequence selected from the group consisting of LK-I (SEQ ID NO:175), LK-V (SEQ ID NO:176), LK-VI (SEQ ID NO:177), LK-VIII (SEQ ID NO:178), Culekinin (SEQ ID NO:179), Ly7linaea lymnokinin (SEQ ID NO:180), DLK-1 (SEQ ID NO:181), DLK-2 (SEQ ID NO:182), and DLK-2a (SEQ ID NO:183); and

DmGPCR8 and an allatostatin that has a sequence with at least 99% sequence identity to a sequence selected from the group consisting of AST-C (SEQ ID NO:184) and DST-C (SEQ ID NO:185).

60 (New). The method according to claim 15, wherein said DmGPCR and said DmGPCR binding partner is selected from the group consisting of:

DmGPCR1 and a DmGPCR1 binding partner has a sequence selected from the group consisting of SEQ ID NO:186 and SEQ ID NO:187;

DmGPCR5 and a drotachykinin that has a sequence selected from the group consisting of DTK-1 (SEQ ID NO:169), Met8-DTK-2 (SEQ ID NO:170), DTK-2 (SEQ ID NO:171), DTK-3 (SEQ ID NO:172), DTK-4 (SEQ ID NO:173), and DTK-5 (SEQ ID NO:174);

DmGPCR7 and a leucokinin that has a sequence selected from the group consisting of LK-I (SEQ ID NO:175), LK-V (SEQ ID NO:176), LK-VI (SEQ ID NO:177), LK-VIII (SEQ ID NO:178), Culekinin (SEQ ID NO:179), Ly7linaea lymnokinin (SEQ ID NO:180), DLK-1 (SEQ ID NO:181), DLK-2 (SEQ ID NO:182), and DLK-2a (SEQ ID NO:183); and

DmGPCR8 and an allatostatin that has a sequence selected from the group consisting of AST-C (SEQ ID NO:184) and DST-C (SEQ ID NO:185).